CATGGGTG	10 GGGGT	GGGG	GCGC	TGC	TGG/	30 4TT(	ССТО	GCTO	CTGG	GTG(	GAG(	50 GGGA		CTT(	GTG/	4GG
GGCTGGTA	70 AGCGC	CCCC	CTCCG	AAG	ССТО	90 GGTG	GTGT	rgce	GCG0	GG(	GA/	11 AGGA		ΓΤΑ(	GTT:	ГСС
TCTCCACC	30 CATGG	GCAC	CCCT	ТСТ		L50 CGGG	GCC	CTGG	ĭGA⊅	GTG	GGG	17 CTGC	-	GTO	GGG(	CAA
ATGCTGGG	90 GCCTC		ATGG/		AGA(							23 CACG R	TGG		\GCT	
29 GCGGAGAG G E S			CCTG <sup>*</sup> P <u>V</u>		CCCA						GCT _L	29 GCT <b>L</b>		iggc _A_	CCC R	GG A
3: CCCAGGGCC Q G (			AGCC( S P		GTG						CTT F	35 CCA H	CAA		GAT I	
37 GTCTGTTT1 L F C	GTTG				AGC		GCA H				GGC A		TTG		GGA E	
43 CCTGCGGCA	ACTCC				GTG								CTG			
C G N 49 ACCATAATT	0				5	10	7		T		L	530	W )	E	N	Н
ACCATAATT H N S	E	C A	A R	C	Q	Α	С	D	E	Q	A	S	Q	у У	A	GC L
55 TGGAGAACT E N C	GTTCA				CAC		CTGT						CTG		TGT( V	
61 AGTGCCAGG C Q V	TCAGC				CAGT								\TG(		AGA( D	

FIG.1A

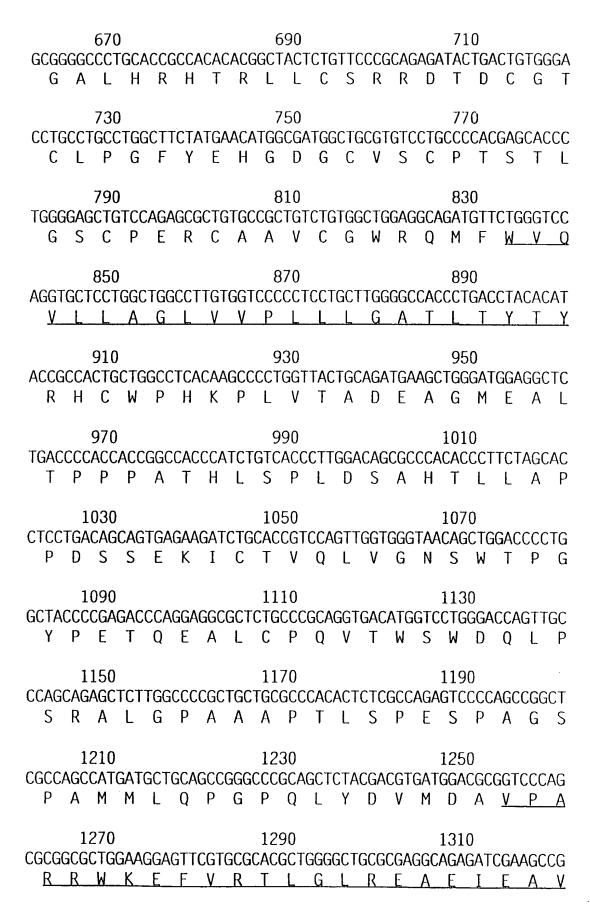


FIG.1B

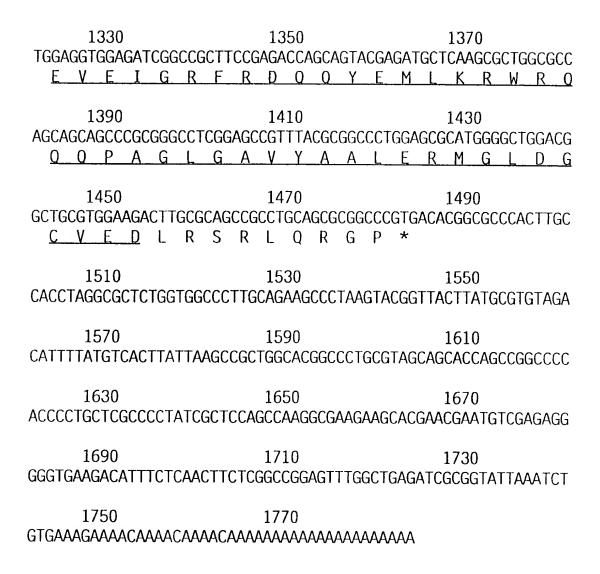


FIG.1C

1	ATG	GA	GCA	\GC	GGCC	:GCG	GGG	CTG	CGC	GGCG	GT	GGC	GGC	GG	CGCT	CCI	ГССТ	GGT	GCT	GCTG
	М	E	Q	R	Р	R	G	С	Α	Α	٧	_A	Α	Α	L	L	L	<u> </u>	L	L
61															ACTG C				CTI F	
121	AAG K			TG G						AGGC G					GGCA H		ACCT L		GGC A	
181				GC P						CTGC C					CCCA Q		ACAC T			
241	TGG W				ACCA H										CCTG C			GCA Q		
301															GCTG C					
361	TGG W						GGT V		CCA Q				CAG S		CACC P		TCTA Y	CTG C		ACCA P
421															TCTG C			CAG R		TACT T
481															ATGG G				CTC C	
541		AG S		CC L	TGGG G	GAG S		TCC. P		GCGC R			CGC <sup>*</sup>		TCTG C	TG( G	GCTG W	GAG R	GCA Q	GATG M
601	TTC F									CCTT L					TCCT L			GGC A		
661															TTAC T					
721															CCTT L					
781	CTT	CT L		AC P	CTCC P					GAAG K					TCCA Q					CAGC S

841	TG( W	GAC T	CCC P	TG G	GCTA Y	CCC P	CGA E	GAC T			GC A			CC P	CGC/ Q	AGG1 V	GAC T	ATC W	GTC S	CTGG W
901	_	CCA Q		GC P	CCAG S	CAG R			TGG G			TGC A			CCA(	CAC1 L	CTC S	GCC P	AGA E	GTCC S
961					CGCC P									GC Q	AGC <sup>*</sup>	_	ACGA D	CG1 V	GAT M	GGAC D
1021	GC(		CCC P	AG A	CGCG R	GCG R	CTG W		GGA E		GT( V	GCG( R	CAC(	GC L	TGG( G	GC1 L	GCG R	CGA E	GGC A	AGAG E
1081			AGC A			GG T				CCGC R				CC Q		AGTA Y				CAAG K
1141	CG( R		GCG( R	CC Q	AGCA Q		GCC P		GGG(			AGC( A		TT Y		CGGC A	CCT L		GCG R	CATG M
1201	GG(		GGA(			CGT(			CTTO		AG(		CCT( L	3C Q	AGCC R	_	CCC	GTG	Α	

FIG.2B

Consensus #1 M		0.00	m m m	m m m		m ~ m
Insus #1 M		22 33	55 55	8 8 8		11 12
sns us	· · · · · · · · · · · · · · · · · · ·	E E T Q Q G E A P R G Q L R G E S A A P V P Q A L L L V G L S T V P D L L L P L V L L E L L V G I Y P S G V I G - L G I W T L L P L V L T S V A R L S S K S V N A Q V T	G A R A Q G G T R S P R C D C A G D F H K K 1 G L F P H L G D R E K R D S V C P Q G K Y 1 H P Q N N S I N S K G L E L R K T V T T V E T Q N L E G L H H D G Q F	 R G C P A G H Y L K A P C T E P C G N S T C L V C P Q D T K C H K G T Y L Y N D C P G P G Q D T D C R E C E S G K P C P P G E R K A R D C T V N G D E P D C V P C Q E G	· · · · · · · · · · · · · · · · · · ·	LAWENHHNSECARCOACDEOASOVALEN TASENHLR-HCLSCSKCRKEMGOVE1SS YTDKAHFSSKCRRCRLCDEGHGLEVEIN
		DDCR TNFR1 FAS	 DDCR TNFR1 FAS	 DDCR TNFR1 FAS		DDCR TNFR1 FAS

FIG. 3A

· · · · · · · · · · · · · · · · · · ·	RCGCKPGWFVECQVSQCVSSS 145 VCGCRKNQYRHYWSENLFQC 144 KCRCKPNFFQN 137		CLDCGALHRHTRLLCSRRDTDCGT 175 CLN-GTVHLSCQEKQNTVCT 167 CEHCDPCTK 148	· · · · · · · · · · · · · · · · · · ·	EHGDGCVSCPTSTLG-SCPERC 203 LRENECVSCSNCKKSLECTKLCLP 197 KECTLTSNTKC 166		- A A V C G W R Q M F W V Q V L L A G L V V P L 225 3 T E D S G T T V L L P L V I F F G L C L L S L 227 - K E E G S R S N L G W L C L L L - L P I P L 186
•	ပြေ			· · · · · · · · · · · · · · · · · · ·	பயல	•	لاس سا
Consensus #1	DDCR TNFR1 FAS	Consensus #1	DDCR TNFR1 FAS	Consensus #1	DDCR TNFR1 FAS	Consensus #1	DDCR TNFR1 FAS

FIG.38

1

	A L 255 K E 256 H R 203		T V 285 F S 286 214		L - 315 V A 315 214		336 S A 345 226
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	A S L		而 C I 저 는 I		N G I ≥ K I		<b>∀</b>
	О 0 П Х Х		SFI		M		
	-		0 0 I		> L I		SZN
	> L - >		4 d l		0 0 I		4-7
	전 다 기업		1 F L				ED S
	A X X H X X		H Q I		д Ф. I		N A S P S P
	니 <u>용 용</u> 니 저 >		AZI SGI				AAT
	9 & I	Д			~ N I		AA -
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		ა	C S S		\(\rangle \) \(\rangle \) \(\rangle \) \(\rangle \)		)   .   V   .
	0 U		9 П S		0 N I		S > 1
			SOX		0 d l		
#1		#1		#1		#1	
Consensus	DDCR TNFR1 FAS	Consensus	DDCR TNFR1 FAS	Consensus	DDCR TNFR1 FAS	Consensus	DDCR TNFR1 FAS

**a**.. **a** 

FIG. 3C

	362 375 249		391 405 279		418 435 308		428 455 335
V 3 . X	PAMMLQPGPQLYDVMDAVPARRWKEFV HKPQSLDTDDPATLYAVVENVPPLRWKEFV DVDLSKYITTIAGVMTLSQVKGFV	I R G 1	RTLGLREAEIEAVEVEIGR-FROOOYEMLK RRLGLSDHEIDRLELONGRCLREAOYSMLA RKNGVNEAKIDEIKNDNVOOTAEOKVOLLR	. w	RWRQQQPAGLGAVYAALERMGLDGCVE TWRRRTPRREATLELLGRVLRDMDLLGCLE NWHQLHGKKEA-YDTLIKDLKKANLCTLAE		OL RSRLQRGP O IEEAL CGPAALPPAPSLLR KIQTIILKDITSOSENSNFRNEIQSLV
Consensus #	DDCR TNFR1 FAS	Consensus #1	DDCR TNFR1 FAS	Consensus #1	DDCR TNFR1 FAS	Consensus #	DDCR TNFR1 FAS

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FIG. 3D

